

RT	McMurray A.;	
RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.	
RT	elegans."	
RL	submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.	
RN	121	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=94150718; PubMed=7906398;	
RA	Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,	
RA	Boxfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,	
RA	Croxton M., Dear S., Du Z., Durbin R., Favellio A., Fulton L.,	
RA	Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,	
RA	Jones M., Keshaw J., Kirsten J., Laister N., Lattelle P.,	
RA	Lightning J., Lloyd C., McMurray A., Morlmore B., O'Callaghan M.,	
RA	Patsons J., Percy C., Riklen L., Roopra A., Saunders D., Shownkeen R.	
RA	Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,	
RA	Therley-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,	
RA	Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;	
RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.	
RT	elegans."	
RL	Nature 368:32-38(1994).	
DR	EMBL; 249886; CAA90055.1; -.	
DR	INTERPRO; IPR000561; -.	
DR	INTERPRO; IPR001007; -.	
DR	INTERPRO; IPR001450; -.	
DR	INTERPRO; IPR001502; -.	
DR	PROSITE; PS00022; EGF_1; UNKNOWN_1.	
DR	PROSITE; PS00198; 4FEAS_FERRDOXIN; UNKNOWN_1.	
DR	PROSITE; PS00764; ENDONUCLEASE_III_1; 1.	
DR	PROSITE; PS01208; VMEC; UNKNOWN_1.	
QO	SEQUENCE 152 AA; 15645 MW; 6E234F0BEA76D354 CRC64;	

Query Match	100.0%;	Score 75;	DB 5;	Length 152;
Best Local Similarity	22.2%;	Pred. NO. 16;		
Matches	6;	Conservative	21;	Mismatches 0;
			Indels	0;
			Gaps	0;

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QY      1  CAXCXXCXXXXXXXXXXCXXCXXC  27
          |::|::|::|::|::|::|::|
Db      88  CTCRCCTRCCTCPCCGCGCGC  114

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RESULT	5			
022048				
ID	022048	PRELIMINARY;	PRT;	164 AA.
DT	01-NOV-1996	(TrEMBLrel. 01, Created)		
DT	01-NOV-1996	(TrEMBLrel. 01, Last sequence update)		
DT	01-MAY-2000	(TrEMBLrel. 13, Last annotation update)		
DE	TO1B7.8	PROTEIN.		
GN	TO1B7.8			
OS	Caenorhabditis elegans			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;			
OC	Rhabditidae; Pelodermidae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
NR	[1]			
RP	SEQUENCE FROM N.A.			
RA	Sims M.;			
RL	Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.			
RP	[2]			
RP	SEQUENCE FROM N.A.			
RA	Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,			
RA	Braxfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,			
RA	Coxford M., Dear S., Du Z., Durbin R., Favella A., Fulton L.,			
RA	James A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,			
RA	Jones M., Keshav J., Kirsten J., Laister N., Latreille P.,			
RA	Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,			
RA	Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,			
RA	Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,			
RA	Therriery-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,			
RA	Watson A., Wellstock L., Wilkinson-Sproat J., Wohlman P.;			
RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans";			

RL Nature 366:32-38(1994)
 DR EMBL: Z66499; CA91301.1; -.
 DR INTERPRO: IPR000561; -.
 DR INTERPRO: IPR001007; -.
 DR INTERPRO: IPR001271; -.
 DR INTERPRO: IPR001450; -.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS00198; 4PE4S_FERREROXIN; UNKNOWN_1.
 DR PROSITE: PS00269; DEFENSIN; UNKNOWN_1.
 DR PROSITE: PS01208; WVEC; UNKNOWN_1.
 SO SEQUENCE 164 AA; 16499 MW; C002048D36C9CECD CRC64

Query Match	100.0%	Score 75;	DB 5;	Length 164;
Best Local Similarity	22.28;	Pred. No. 17;		
Matches	6;	Conservative 21;	Mismatches 0;	Indels 0;
			Gaps	0;

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QY      1 CXXCXXCXXCXXCXXCXXCXXCXXC 27
          |::|::|::|::|::|::|::|
Db      84 CCCCPRCCCCCRRCTCCRTCCCTR 110
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ESU	PT	6	18238	18238
D	018238	PRELIMINARY;	PT; 188	AA.
C	018238;			
T	01-NOV-1996	(TREMblrel. 01, Created)		
T	01-NOV-1996	(TREMblrel. 01, Last sequence update)		
T	01-OCT-2000	(TREMblrel. 15, Last annotation update)		
E	COSMID C27A2.			
N	C27A2.5.			
S	Caenorhabditis elegans.			
C	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditicoidea			
C	Rhabditidae; Pelodermidae; Caenorhabditis.			
X	NCBI_TaxID=6239;			

SEQUENCE FROM N.A.
C STRAIN-BRISTOL N2;
X MEDLINE=94150718; PubMed=7906398;
X Wilson R., Alnsough R., Anderson K.,
A Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
A Craxton M., Dear S., Du Z., Durbin R., Favetto A., Fulton L.,
A Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
A Jones M., Kershaw J., Kirsten T., Laister N., Latreille P.,
A Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
A Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
A Smaldon N., Smith A., Sonhammer E., Straden R., Sulston J.,
A Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
A Watson A., Weinstock L., Wilksinson-Spratt J., Woollam P.;
T "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C.*
T *elegans* ";
T Nature 368:32-38(1994).

Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases

RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2:
RA Submitted R :
RL Submitted (MAY 1996) to the EMBL/Genbank/DBJ databases
DR EMBL: U58760; AAB00710.1; -;
DR INTERPRO: IPR001007; -;
DR INTERPRO: IPR001271; -;
DR INTERPRO: IPR001450; -;
DR PROSITE: PS00198; 4FAS_PEPREDOXIN; UNKNOWN_1.
DR PROSITE: PS00269; DEENSN; 1.
DR PROSITE: PS01208; VWC; UNKNOWN_1.
QO SEQUENCE 188 AA; 18878 MW; 0C5DD0DC5CABE0C4B CRC64;

Query Match	100.0%; Score 75; DB 5; Length 188;
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RP SEQUENCE FROM N.A.
RA Kuech A., Buemann H.;
RL Submitted (DEC-1990) to the EMBL/GenBank/DBJ databases.
DR EMBL; X58114; CA41118.1; -;
DR FLBASE: FBgn0015097; DnydMst87Fp.
DR INTERPRO: IPR001450; -;
DR PROSITE: PS00198; 4P4S_FERREDOXIN; UNKNOWN_1.
SO SEQUENCE 49 AA; 4550 MW; 24758ECC136FID CRC64;

Query Match	88.0%;	Score 66;	DB 5;	Length 49;
Best Local Similarity	19.2%;	Pred. No. 46;		
Matches 5;	Conservative 21;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

RESULT	11	
Q92044		
ID	Q92044	PRELIMINARY;
		PRT;
		60 AA

DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE METALLOTHIONEIN (MT).
 GN MT A.
 OS *Cyprinodon* sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ruteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC *Cyprinodontiformes*; Cyprinodontidae; Cyprinodon.

PN SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RA Kille P., Olsson P.E.;
RL submitted (AR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE PROTEINS ARE
CC TRANSCRIPTIONALLY REGULATED BY BOTH HEAVY METALS AND
CC GLUCOCORTICOIDS.

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DR      LMBU, A51213, CA050526.1; -.
DR      HSSP; P02802; IDES.
DR      INTERPRO; IPR000006; -.
DR      INTERPRO; IPR003019; -.
DR      PFAM; PF00131; metalthio; 1.
DR      PRINTS; PR00860; MTVERTEBRATE
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DR PROSITE; PS00203; METALLOTHIONEIN_VRT; 1.
KW Metal-binding; Metal-thiolate cluster; Chelation; Zinc

	60 AA;	6093 MW;	F73A5EEB39CDBD971	CRC64
FT METAL.	14	16	CLUSTER.	
FT METAL.	18	18	CLUSTER.	
FT METAL.	20	20	CLUSTER.	
FT METAL.	21	21	CLUSTER.	
FT METAL.	23	23	CLUSTER.	
FT METAL.	25	25	CLUSTER.	
FT METAL.	26	26	CLUSTER.	
FT METAL.	28	28	CLUSTER.	
FT METAL.	30	30	CLUSTER.	
SEQUENCE				

Query Match	88.0%;	Score 66;	DB 13;	Length 60;
Best Local Similarity	19.2%;	Pred. NO. 52;		
Matches	5;	Conservative	21;	Mismatches 0;
			Indels	0;
			Gaps	0

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QY      1 CXXCXXXCX XXXXXXXX CX XXXCXX 26
        |::|::|::|::|::|::|::|::|::|::
Db     25 CKCKKSCCSCCP SGC SKCASCVC 50
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RESULT 12
073914

ID	073914	PRELIMINARY;	PRT;	60 AA.
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DT 01-AUG-1998 (TREMBLRE). 07, Created)

DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update, NCBI/EMBL/GENBANK/DBP)

	G.N.	M.T.
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05 Notothenia coriiceps neglecta (Black rockcod) (Yellowbelly rockcod)
05 and Chionodrao rastrosipinosus.

0C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
0C Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

CC Acantlinoidea; Acantliopterygia; percomorpha; perciformes;
CC Nototheniidae; Nototheniidae; Notothenia.
CC Nototheniidae; Nototheniidae; Notothenia.
CC Nototheniidae; Nototheniidae; Notothenia.

NCBI_TaxID=8209, 34790;

RP SEQUENCE FROM N. A.

RA Scudiero R., Verde C., Carginale V., Capasso C., di Prisco G.
RA Parisi E.;

Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.
PC TISSUE-TYPE.

RA
Cargiale V., Capasso C., Scudiero R., Parisi E.;
"Metallothionein in Antarctic Organisms".
UNIVERSITY OF NAPLES, ITALY

Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases

RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE PROTEINS ARE TRANSCRIPTIONALLY REGULATED BY BOTH HEAVY METALS AND

IRONOCALFICIONNELI REGULATED BY BOTH HEAVY METALS AND
GLUCOCORTICOIDS.
EMRI : A1006484 - CAA07063 1. -

DR	EMBL; F03000404; CAA07003.1;
DR	EMBL; AJ011584; CAA09714.1; -.
DR	HSSP: P02802. 1 DES

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DR      ADDR / 102002, ID10:
DR      INTERPRO; IPR000006; -.
DR      INTERPRO; IPR003019; -
```

DR PFAM; PF00131; metalthio; 1
DR PRINTS: PR00860: MTFEPTERRA

DR PROSITE; PS00203; METALLOTHIONEIN_VRT; 1.
Metal-binding: Metal-thiolate cluster; Chelation; zinc

METAL	23	CLUSTER.
FT METAL.	26	CLUSTER

F1	METAL	20	20	CLUSTER
F2	METAL	16	16	CLUSTER
F3	METAL	18	18	CLUSTER

ET	METAL	30	30	CLUSTER
FT	METAL	21	21	CLUSTER.
ET	METAL	18	18	CLUSTER

SEQ	SEQUENCE	60 AA;	6019 MW;	E866E7155A2C424A CRC64;
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Query Match	88.0%;	Score 66;	DB 13;	Length 60;
Best Local Similarity	19.2%;	Pred. No. 52;		
Matches	5; Conservative	21; Mismatches	0; Indels	0; Gaps

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QY      1  CXXCXXXXCXXXXXXCXXCXXCXX  26
          |::|::|::|::|::|::|::|::|
Db     25  CKSCCKSCCPCPSGCTKCAAGCVCK  50

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RESULT 13

093593 ID 093593 PRELIMINARY; PRT; 60 AA

AC	093593;
DT	01-NOV-1998 (TREMBLE). 08, Created)

DT	DT
01-NOV-1998	(TREMBLrel. 08, Last sequence update)
01-OCT-2000	(TREMBLrel. 15, Last annotation update)

DE METALLOPHONEIN (MT) :
GN MT.

05 Chaenocephalus aceratus;
0C Eukaryota; Metazoa; Chordata; Vertebrata; Pisces; Clupeiformes; Clupeidae; Clupea

0C Actinopterygii: Neopterygii; Teleostei; Euteleostei; Neoteleostei
0C Acanthomorpha: Acanthopterygii; Percomorpha; Perciformes;

0C Notothenioidae; Chaenicephalus.
0X NCBI_TaxID=36190;

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA "Metallothionein in Antarctic organisms.";
RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE PROTEINS ARE
TRANSCRIPTIONALLY REGULATED BY BOTH HEAVY METALS AND
GLUCOCORTICOIDS.
CC EMBL: AJ011583; CA09713.1; -.
DR HSSP: P02802; 1DFS.
DR INTERPRO: IPR000006; -.
DR INTERPRO: IPR003019; -.
DR PFAM: PF00131; metalthio. 1.
DR PRINTS: PR00860; MTVERTERATE.
DR PROSITE: PS00203; METALLOTHIONEIN_VRT; 1.
KM Metal-binding: Metal-thiolate cluster; Chelation; Zinc.
FT METAL 23 23 CLUSTER.
FT METAL 26 26 CLUSTER.
FT METAL 16 16 CLUSTER.
FT METAL 18 18 CLUSTER.
FT METAL 21 21 CLUSTER.
FT METAL 30 30 CLUSTER.
SQ SEQUENCE 60 AA; 6017 MW; E8773344264C424A CRC64;

Query Match 88.0%; Score 66; DB 13; Length 60;
Best Local Similarity 19.2%; Pred. No. 52;
Matches 5; Conservative 21; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXCXXXXXXCXXCXXCXX 26
DB 25 CKSKKSCPCPCPCGCKKCAAGCVCI 50

RESULT 14
093609 PRELIMINARY; PRT; 60 AA.
ID 093609;
AC 093609;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE METALLOTHIONEIN (MT).
GN MT.
OS Trematomus bernacchii.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Perciliformes;
OC Notothenioidae; Nototheniidae; Trematomus.
OX NCBI_TaxID=40690;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA "Metallothionein in Antarctic organisms.";
RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE PROTEINS ARE
TRANSCRIPTIONALLY REGULATED BY BOTH HEAVY METALS AND
GLUCOCORTICOIDS.
CC EMBL: AJ011583; CA09713.1; -.
DR HSSP: P02802; 1DFS.
DR INTERPRO: IPR000006; -.
DR INTERPRO: IPR003019; -.
DR PFAM: PF00131; metalthio. 1.
DR PRINTS: PR00860; MTVERTERATE.
DR PROSITE: PS00203; METALLOTHIONEIN_VRT; 1.
KM Metal-binding: Metal-thiolate cluster; Chelation; Zinc.
FT METAL 23 23 CLUSTER.
FT METAL 26 26 CLUSTER.
FT METAL 16 16 CLUSTER.
FT METAL 18 18 CLUSTER.

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FT METAL 21 21 CLUSTER.
FT METAL 30 30 CLUSTER.
SQ SEQUENCE 60 AA; 6018 MW; AC66F3015A2C4251 CRC64;

Query Match 88.0%; Score 66; DB 13; Length 60;
Best Local Similarity 19.2%; Pred. No. 52;
Matches 5; Conservative 21; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXCXXXXXXCXXCXXCXX 26
DB 25 CKSKKSCPCPCPCGCKKCAAGCVCK 50

RESULT 15
013259 PRELIMINARY; PRT; 60 AA.
ID 013259;
AC 013259;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE METALLOTHIONEIN (MT).
GN MTB.
OS Chionodraco hamatus, Morone saxatilis (Striped bass), and
OS Gymnodraco acuticeps.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Perciliformes;
OC Notothenioidae; Channichthyidae; Chionodraco.
OX NCBI_TaxID=36188, 34816, 8218;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=C.hamatus;
RA "Cardinale V., Scudiero R., Capasso A., Capasso C., Kille P.,
di Prisco G., Parisi E.;
Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.saxatilis;
RA "Leclerc G.M., Leclerc G.J., Ely B.;
Molecular cloning of the striped bass (Morone saxatilis)
metallothionein gene (sbMT).";
RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=G.acuticeps, and M.saxatilis; TISSUE=LIVER;
RA "Cardinale V., Scudiero R., Capasso C., Parisi E.;
Metallothioneins in Antarctic fish.";
RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE PROTEINS ARE
TRANSCRIPTIONALLY REGULATED BY BOTH HEAVY METALS AND
GLUCOCORTICOIDS.
CC EMBL: Y12581; CAAT3160.1; -.
DR EMBL: AF091100; AAC62501.1; -.
DR EMBL: AJ007561; CA07556.1; -.
DR HSSP: P02802; 1DFS.
DR INTERPRO: IPR000006; -.
DR INTERPRO: IPR003019; -.
DR PFAM: PF00131; metalthio. 1.
DR PRINTS: PR00860; MTVERTERATE.
DR PROSITE: PS00203; METALLOTHIONEIN_VRT; 1.
KM Metal-binding: Metal-thiolate cluster; Chelation; Zinc.
FT METAL 14 14 CLUSTER.
FT METAL 16 16 CLUSTER.
FT METAL 18 18 CLUSTER.
FT METAL 20 20 CLUSTER.
FT METAL 21 21 CLUSTER.
FT METAL 23 23 CLUSTER.
FT METAL 25 25 CLUSTER.
FT METAL 26 26 CLUSTER.
FT METAL 28 28 CLUSTER.
FT METAL 30 30 CLUSTER.

```

SQ SEQUENCE 60 AA; 5978 MW; 5966F5AC61BC424B CRC64;

Query Match	88.0%;	Score 66;	DB 13;	Length 60;
Best Local Similarity	19.2%;	Pred. NO. 52;		
Matches	5;	Conservative 21;	Mismatches 0;	Indels 0;
				Gaps 0;

```
Qy      1 CXXCXXXXXXXXXXXXCXXCXX 26
Db      25 CTSCCKSCPCPCPGCTKCAAGCVCK 50
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Search completed: March 1, 2001, 16:22:04
Job time: 281 sec
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